

SEQUENCE LISTING

<110> Dumas, Renaud
 Lebrun, Marc-Henri
 Zundel, Jean-Luc
 Effantin, Géraldine
 Morin, Valérie

<120> Use of inhibitors of ketol-acid reductoisomerase to prevent or treat fungal infection of plants

<130> A36156-PCT-USA-A 072667.0196

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<212> PRT

<213> Magnaporthe grisea

<220>

<221> TRANSIT

<222> (1)..(51)

<223> Putative mitochondrial transit peptide

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Met	Val	Arg	Ala	Thr	Arg	Lys	Ala	Ala	Val	Ala	Pro	Thr	Gln	Gln	Gln
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Ile	Arg	Gly	Val	Lys	Thr	Met	Asp	Phe	Ala	Gly	His	Lys	Glu	Gln	Val
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Trp	Glu	Arg	Ala	Asp	Trp	Pro	Lys	Glu	Lys	Leu	Leu	Glu	Tyr	Phe	Lys
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Asp	Asp	Thr	Leu	Ala	Leu	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His	Gly	Gln
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Gly	Leu	Asn	Leu	Arg	Asp	Asn	Gly	Leu	Asn	Val	Ile	Ile	Gly	Val	Arg
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Lys	Asp	Gly	Lys	Ser	Trp	Lys	Asp	Ala	Val	Gln	Asp	Gly	Trp	Val	Pro
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 Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg
 195 200 205
 Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr
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 Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val
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 Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His
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 Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser
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 325 330 335
 Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp
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 Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr
 355 360 365
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<213> *Saccharomyces cerevisiae*

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<223> mitochondrial transit peptide

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<309> 1993-09-12

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Ala	Cys	Ser	Thr	Thr	Ala	Arg	Arg	Gly	Ala	Ile	Asp	Trp	Thr	Pro	Lys	
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Phe	Lys	Asp	Ala	Leu	Lys	Pro	Val	Phe	Asn	Asn	Leu	Tyr	Asp	Ser	Val	
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 Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln Leu Ala Thr Pro
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 Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ser Ser Met Val Arg Ala
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 acc agg aaa gcc gcc gtc gct ccc act cag cag cag atc cgt ggt gtc 199
 Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln Ile Arg Gly Val
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 aag acc atg gat ttt gct ggc cac aag gag cag gtc tgg gag cgt gcc 247
 Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val Trp Glu Arg Ala
 55 60 65
 gac tgg ccc aag gag aag ctg ctg gag tac ttc aag gac gac acc ctt 295
 Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys Asp Asp Thr Leu
 70 75 80

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Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln Gly Leu Asn Leu	
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cgc gac aac ggc ctc aac gtc atc atc ggt gtg cgc aag gac gga aag	391
Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Lys	
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tgc tgg aag gac gcc gtc cag gac ggc tgg gtt ccc ggc aag aac ctc	439
Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro Gly Lys Asn Leu	
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ttc gag gtc gac gag gcc atc tgc cgc ggt acc gtc atc atg aac ctt	487
Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val Ile Met Asn Leu	
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ctg agc gac gct gcc cag agc gag acg tgg cct gct ctg aag ccc cag	535
Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Leu Lys Pro Gln	
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atc act aag ggc aag act ctc tac ttc tgc cac ggt ttc tct ccc gtc	583
Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val	
165 170 175 180	
ttc aag gac ctc acc aag gtc gag gtc ccc acc gac gtc gac gtc atc	631
Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp Val Asp Val Ile	
185 190 195	
ctc tgc gcc ccc aag ggc tcc ggc cgc act gtc cgc tgc ctc ttc cgc	679
Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Arg	
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Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val Ala Ile Gly Ser	
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Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val Tyr Ser Asp Leu	
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Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu	
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Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser Pro Ser Glu Ala	
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ttc aac gag act gtc gag gag gcc acc cag tct ctc tac ccc ctg atc	967
Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile	
295 300 305	
ggt gcc aac ggc atg gac tgg atg tac gag gcc tgc tct acc act gct	1015

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Ile	Arg	Gly	Val	Lys	Thr	Met	Asp	Phe	Ala	Gly	His	Lys	Glu	Gln	Val	
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Trp	Glu	Arg	Ala	Asp	Trp	Pro	Lys	Glu	Lys	Leu	Leu	Glu	Tyr	Phe	Lys	
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